

SUPPLEMENTAL INFORMATION

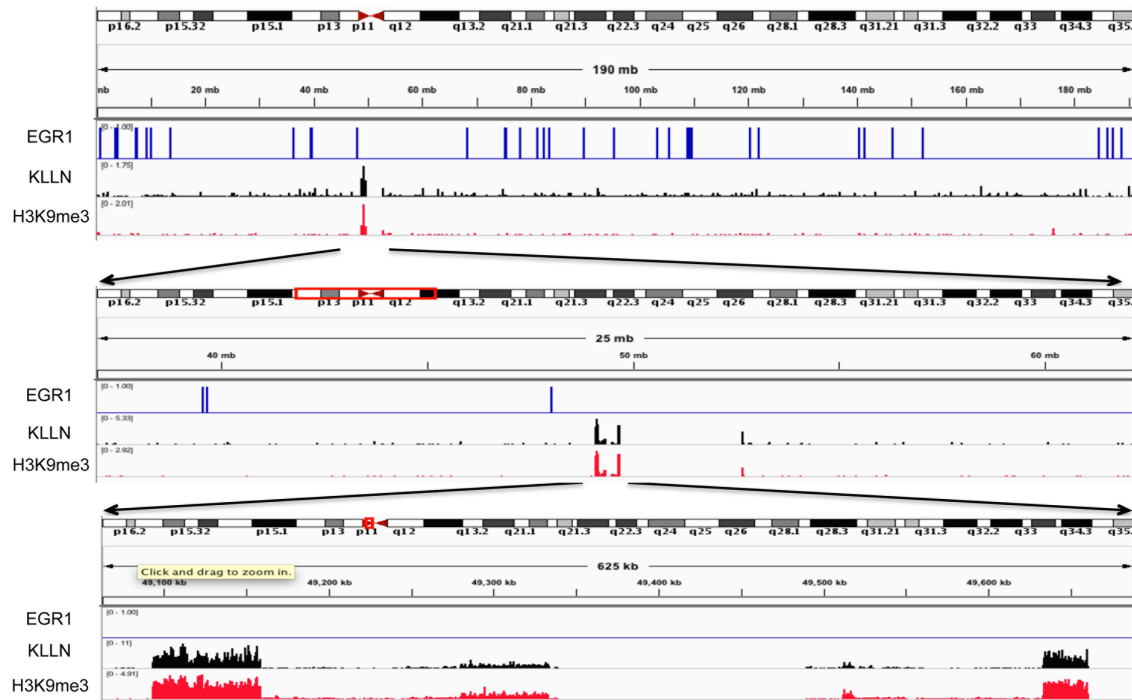
TITLE: Cancer-predisposition gene *KLLN* maintains pericentric H3K9 trimethylation protecting genomic stability

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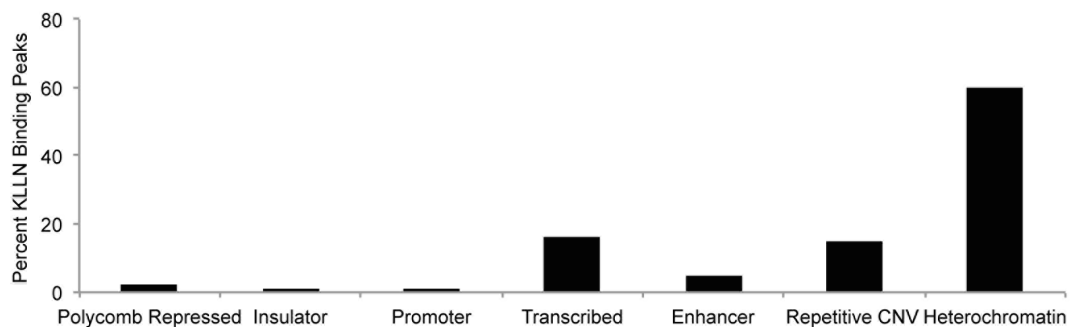
Supplementary Figures and Legends

Figure S1.



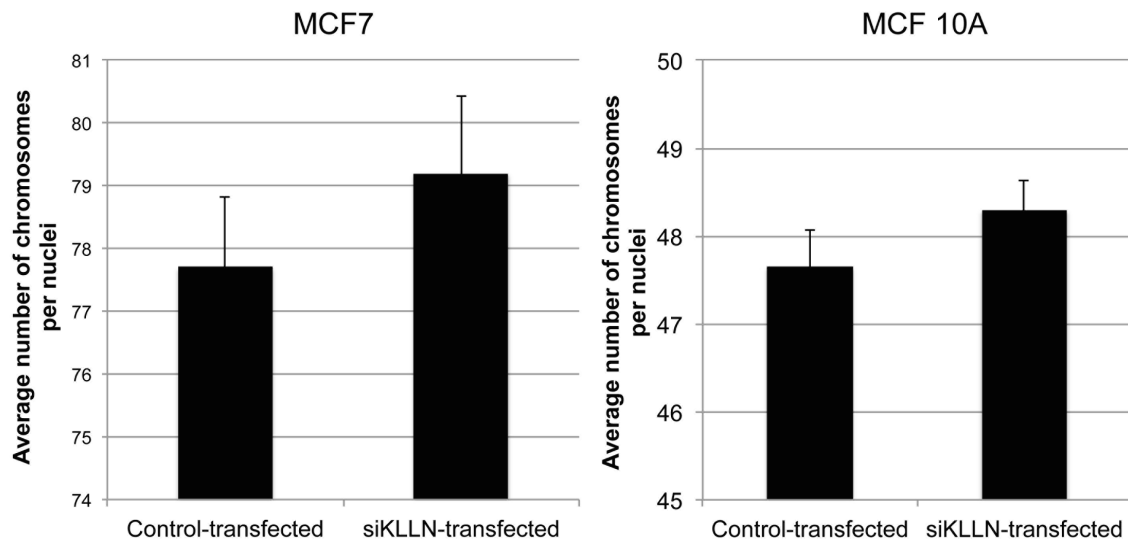
Supplementary Figure S1. KLLN, EGR1 and H3K9me3 binding sites. IGV screen shots of peaks from ChIP-seq data for KLLN, EGR1 and histone mark H3K9me3. The upper panel represents an individual chromosome and the bottom panels are zoomed in to show the centromeric region. H3K9me3 and KLLN peaks overlap consistently, whereas there is no observable overlap between neither H3K9me3 and EGR1 nor KLLN and EGR1.

Figure S2.



Supplementary Figure S2. KLLN binding sites and chromatin states. Bar graph of percentage of KLLN binding peaks, which fall within different chromatin states defined by a combination of histone modifications in HMECs. The majority of KLLN binding peaks fall within regions of heterochromatin.

Figure S3.



Supplementary Figure S3. Numerical chromosomal aberrations. Bar graphs of average number of chromosomes counted per nuclei with and without knockdown of KLLN in MCF7 and MCF10A cells. Knockdown of KLLN increased the number of chromosomes per nuclei in both cell lines.

Supplementary Tables

Table S1. Quality measures for KLLN ChIP-seq data

ChIP Samples	# of Reads	# of Bases	Average Quality	% Most Abundant Duplicate	% Passed Filter
KLLN1	174,705,151	8,735,257,550	37	0.022	82
KLLN2	158,515,802	7,925,790,100	37	0.022	81
Input KLLN1	174,593,448	8,729,672,400	37	0.020	82
Input KLLN2	161,231,627	8,061,581,350	37	0.030	81

Table S2. GO terms associated with gene networks regulated by both KLLN and H3K9me3

TermID	Term	Enrichment	logP
GO:0009987	cellular process	4.12E-07	-14.70234799
GO:0007154	cell communication	1.66E-06	-13.30860053
GO:0044763	single-organism cellular process	5.39E-06	-12.13078957
GO:0051897	positive regulation of protein kinase B signaling cascade	1.15E-05	-11.37739001
GO:0048731	system development	1.65E-05	-11.0127408
GO:0007175	negative regulation of epidermal growth factor-activated receptor activity	1.98E-05	-10.83084497
GO:0051270	regulation of cellular component movement	2.00E-05	-10.81777944
GO:0044700	single organism signaling	2.24E-05	-10.70724701
GO:0023052	signaling	2.24E-05	-10.70672171
GO:0044699	single-organism process	2.29E-05	-10.68548879
GO:0051896	regulation of protein kinase B signaling cascade	3.28E-05	-10.32518845
GO:0007420	brain development	4.69E-05	-9.967057122
GO:2000272	negative regulation of receptor activity	5.03E-05	-9.896838849
GO:0061099	negative regulation of protein tyrosine kinase activity	6.01E-05	-9.718734708
GO:0050820	positive regulation of coagulation	7.31E-05	-9.524165191
GO:0048856	anatomical structure development	8.89E-05	-9.328515973
GO:0048583	regulation of response to stimulus	9.43E-05	-9.269216334
GO:0007176	regulation of epidermal growth factor-activated receptor activity	0.000105323	-9.158481959